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RAW SEQUENCE LISTING  
PATENT APPLICATION: US/10/077,054

DATE: 03/04/2002  
TIME: 14:55:07

Input Set : A:\Sequence.app  
Output Set: N:\CRF3\03042002\J077054.raw

3 <110> APPLICANT: Makielski, Jonathan C  
4 Ye, Bin  
6 <120> TITLE OF INVENTION: Sodium Channel Alpha Subunits  
8 <130> FILE REFERENCE: 960296.98032  
C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/077,054  
C--> 11 <141> CURRENT FILING DATE: 2002-02-12  
13 <160> NUMBER OF SEQ ID NOS: 10  
15 <170> SOFTWARE: PatentIn Ver. 2.1  
17 <210> SEQ ID NO: 1  
18 <211> LENGTH: 6091  
19 <212> TYPE: DNA  
20 <213> ORGANISM: Homo sapiens  
22 <220> FEATURE:  
23 <221> NAME/KEY: CDS  
24 <222> LOCATION: (10)..(6054)  
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27 gatgagaag atg gca aac ttc cta tta cct cgg ggc acc agc agc ttc cgc 51  
28 Met Ala Asn Phe Leu Leu Pro Arg Gly Thr Ser Ser Phe Arg  
29 1 5 10  
30 agg ttc aca cgg gag tcc ctg gca gcc atc gag aag cgc atg gcg gag 99  
32 Arg Phe Thr Arg Glu Ser Leu Ala Ala Ile Glu Lys Arg Met Ala Glu  
33 15 20 25 30  
35 aag caa gcc cgc ggc tca acc acc ttg cag gag agc cga gag ggg ctg 147  
36 Lys Gln Ala Arg Gly Ser Thr Thr Leu Gln Glu Ser Arg Glu Gly Leu  
37 35 40 45  
39 ccc gag gag gct ccc cgg ccc cag ctg gac ctg cag gcc tcc aaa 195  
40 Pro Glu Glu Ala Pro Arg Pro Gln Leu Asp Leu Gln Ala Ser Lys  
41 50 55 60  
43 aag ctg cca gat ctc tat ggc aat cca ccc caa gag ctc atc gga gag 243  
44 Lys Leu Pro Asp Leu Tyr Gly Asn Pro Pro Gln Glu Leu Ile Gly Glu  
45 65 70 75  
47 ccc ctg gag gac ctg gac ccc ttc tat agc acc caa aag act ttc atc 291  
48 Pro Leu Glu Asp Leu Asp Pro Phe Tyr Ser Thr Gln Lys Thr Phe Ile  
49 80 85 90  
51 gta ctg aat aaa ggc aag acc atc ttc cgg ttc agt gcc acc aac gcc 339  
52 Val Leu Asn Lys Gly Lys Thr Ile Phe Arg Phe Ser Ala Thr Asn Ala  
53 95 100 105 110  
55 ttg tat gtc ctc agt ccc ttc cac ccc atc cgg aga gcg gct gtg aag 387  
56 Leu Tyr Val Leu Ser Pro Phe His Pro Ile Arg Arg Ala Ala Val Lys  
57 115 120 125  
59 att ctg gtt cac tcg ctc ttc aac atg ctc atc atg tgc acc atc ctc 435  
60 Ile Leu Val His Ser Leu Phe Asn Met Leu Ile Met Cys Thr Ile Leu  
61 130 135 140

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63 acc aac tgc gtg ttc atg gcc cag cac gac cct cca ccc tgg acc aag	483
64 Thr Asn Cys Val Phe Met Ala Gln His Asp Pro Pro Pro Trp Thr Lys	
65 145 150 155	
67 tat gtc gag tac acc ttc acc gcc att tac acc ttt gag tct ctg gtc	531
68 Tyr Val Glu Tyr Thr Phe Thr Ala Ile Tyr Thr Phe Glu Ser Leu Val	
69 160 165 170	
71 aag att ctg gct cga ggc ttc tgc ctg cac gcg ttc act ttc ctt cgg	579
72 Lys Ile Leu Ala Arg Gly Phe Cys Leu His Ala Phe Thr Phe Leu Arg	
73 175 180 185 190	
75 gac cca tgg aac tgg ctg gac ttt agt gtg att atc atg gca tac aca	627
76 Asp Pro Trp Asn Trp Leu Asp Phe Ser Val Ile Ile Met Ala Tyr Thr	
77 195 200 205	
79 act gaa ttt gtg gac ctg ggc aat gtc tca gcc tta cgc acc ttc cga	675
80 Thr Glu Phe Val Asp Leu Gly Asn Val Ser Ala Leu Arg Thr Phe Arg	
81 210 215 220	
83 gtc ctc cgg gcc ctg aaa act ata tca gtc att tca ggg ctg aag acc	723
84 Val Leu Arg Ala Leu Lys Thr Ile Ser Val Ile Ser Gly Leu Lys Thr	
85 225 230 235	
87 atc gtg ggg gcc ctg atc cag tct gtg aag aag ctg gct gat gtg atg	771
88 Ile Val Gly Ala Leu Ile Gln Ser Val Lys Lys Leu Ala Asp Val Met	
89 240 245 250	
91 gtc ctc aca gtc ttc tgc ctc agc gtc ttt gcc ctc atc ggc ctg cag	819
92 Val Leu Thr Val Phe Cys Leu Ser Val Phe Ala Leu Ile Gly Leu Gln	
93 255 260 265 270	
95 ctc ttc atg ggc aac cta agg cac aag tgc gtg cgc aac ttc aca gcg	867
96 Leu Phe Met Gly Asn Leu Arg His Lys Cys Val Arg Asn Phe Thr Ala	
97 275 280 285	
99 ctc aac ggc acc aac ggc tcc gtg gag gcc gac ggc ttg gtc tgg gaa	915
100 Leu Asn Gly Thr Asn Gly Ser Val Glu Ala Asp Gly Leu Val Trp Glu	
101 290 295 300	
103 tcc ctg gac ctt tac ctc agt gat cca gaa aat tac ctg ctc aag aac	963
104 Ser Leu Asp Leu Tyr Leu Ser Asp Pro Glu Asn Tyr Leu Leu Lys Asn	
105 305 310 315	
107 ggc acc tct gat gtg tta ctg tgt ggg aac agc agc tct gac gct ggg aca	1011
108 Gly Thr Ser Asp Val Leu Leu Cys Gly Asn Ser Ser Asp Ala Gly Thr	
109 320 325 330	
111 tgt ccg gag ggc tac cgg tgc cta aag gca ggc gag aac ccc gac cac	1059
112 Cys Pro Glu Gly Tyr Arg Cys Leu Lys Ala Gly Glu Asn Pro Asp His	
113 335 340 345 350	
115 ggc tac acc agc ttc gat tcc ttt gcc tgg gcc ttt ctt gca ctc ttc	1107
116 Gly Tyr Thr Ser Phe Asp Ser Phe Ala Trp Ala Phe Leu Ala Leu Phe	
117 355 360 365	
119 cgc ctg atg acg cag gac tgc tgg gag cgc ctc tat cag cag acc ctc	1155
120 Arg Leu Met Thr Gln Asp Cys Trp Glu Arg Leu Tyr Gln Gln Thr Leu	
121 370 375 380	
123 agg tcc gca ggg aag atc tac atg atc ttc ttc atg ctt gtc atc ttc	1203
124 Arg Ser Ala Gly Lys Ile Tyr Met Ile Phe Phe Met Leu Val Ile Phe	
125 385 390 395	
127 ctg ggg tcc ttc tac ctg gtg aac ctg atc ctg gcc gtg gtc gca atg	1251

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128 Leu Gly Ser Phe Tyr Leu Val Asn Leu Ile Leu Ala Val Val Ala Met			
129 400	405	410	
131 gcc tat gag gag caa aac caa gcc acc atc gct gag acc gag gag aag			1299
132 Ala Tyr Glu Glu Gln Asn Gln Ala Thr Ile Ala Glu Thr Glu Glu Lys			
133 415	420	425	430
135 gaa aag cgc ttc cag gag gcc atg gaa atg ctc aag aaa gaa cac gag			1347
136 Glu Lys Arg Phe Gln Glu Ala Met Glu Met Leu Lys Lys Glu His Glu			
137 435	440	445	
139 gcc ctc acc atc agg ggt gtg gat acc gtg tcc cgt agc tcc ttg gag			1395
140 Ala Leu Thr Ile Arg Gly Val Asp Thr Val Ser Arg Ser Ser Leu Glu			
141 450	455	460	
143 atg tcc cct ttg gcc cca gta aac agc cat gag aga aga agc aag agg			1443
144 Met Ser Pro Leu Ala Pro Val Asn Ser His Glu Arg Arg Ser Lys Arg			
145 465	470	475	
147 aga aaa cgg atg tct tca gga act gag gag tgt ggg gag gac agg ctc			1491
148 Arg Lys Arg Met Ser Ser Gly Thr Glu Glu Cys Gly Glu Asp Arg Leu			
149 480	485	490	
151 ccc aag tct gac tca gaa gat ggt ccc aga gca atg aat cat ctc agc			1539
152 Pro Lys Ser Asp Ser Glu Asp Gly Pro Arg Ala Met Asn His Leu Ser			
153 495	500	505	510
155 ctc acc cgt ggc ctc agc agg act tct atg aag cca cgt tcc agc cgc			1587
156 Leu Thr Arg Gly Leu Ser Arg Thr Ser Met Lys Pro Arg Ser Ser Arg			
157 515	520	525	
159 ggg agc att ttc acc ttt cgc agg cga gac ctg ggt tct gaa gca gat			1635
160 Gly Ser Ile Phe Thr Phe Arg Arg Asp Leu Gly Ser Glu Ala Asp			
161 530	535	540	
163 ttt gca gat gat gaa aac agc aca gcg ggg gag agc gag agc cac cgc			1683
164 Phe Ala Asp Asp Glu Asn Ser Thr Ala Gly Glu Ser Glu Ser His Arg			
165 545	550	555	
167 aca tca ctg ctg gtg ccc tgg ccc ctg cgc cgg acc agt gcc cag gga			1731
168 Thr Ser Leu Leu Val Pro Trp Pro Leu Arg Arg Thr Ser Ala Gln Gly			
169 560	565	570	
171 cag ccc agt ccc gga acc tcg gct cct ggc cac gcc ctc cat ggc aaa			1779
172 Gln Pro Ser Pro Gly Thr Ser Ala Pro Gly His Ala Leu His Gly Lys			
173 575	580	585	590
175 aag aac agc act gtg gac tgc aat ggg gtg gtc tca tta ctg ggg gca			1827
176 Lys Asn Ser Thr Val Asp Cys Asn Gly Val Val Ser Leu Leu Gly Ala			
177 595	600	605	
179 ggc gac cca gag gcc aca tcc cca gga agc cac atc ctc cgc cct gtg			1875
180 Gly Asp Pro Glu Ala Thr Ser Pro Gly Ser His Ile Leu Arg Pro Val			
181 610	615	620	
183 atg cta gag cac ccc cca gac acg acc acg cca tcg gag gag cca ggc			1923
184 Met Leu Glu His Pro Pro Asp Thr Thr Pro Ser Glu Glu Pro Gly			
185 625	630	635	
187 ggg ccc cag atg ctg acc tcc cag gct ccc tgt gta gat ggc ttc gag			1971
188 Gly Pro Gln Met Leu Thr Ser Gln Ala Pro Cys Val Asp Gly Phe Glu			
189 640	645	650	
191 gag cca gga gca cgg cag cgg gcc ctc agc gca gtc agc gtc ctc acc			2019
192 Glu Pro Gly Ala Arg Gln Arg Ala Leu Ser Ala Val Ser Val Leu Thr			

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193	655	660	665	670	
195	agc gca ctg gaa gag tta gag gag tct cgc cac aag tgt cca cca tgc				2067
196	Ser Ala Leu Glu Glu Leu Glu Glu Ser Arg His Lys Cys Pro Pro Cys				
197	675	680	685		
199	tgg aac cgt ctc gcc cag cgc tac ctg atc tgg gag tgc tgc ccg ctg				2115
200	Trp Asn Arg Leu Ala Gln Arg Tyr Leu Ile Trp Glu Cys Cys Pro Leu				
201	690	695	700		
203	tgg atg tcc atc aag cag gga gtg aag ttg gtg gtc atg gac ccg ttt				2163
204	Trp Met Ser Ile Lys Gln Gly Val Lys Leu Val Val Met Asp Pro Phe				
205	705	710	715		
207	act gac ctc acc atc act atg tgc atc gta ctc aac aca ctc ttc atg				2211
208	Thr Asp Leu Thr Ile Thr Met Cys Ile Val Leu Asn Thr Leu Phe Met				
209	720	725	730		
211	gcg ctg gag cac tac aac atg aca agt gaa ttc gag gag atg ctg cag				2259
212	Ala Leu Glu His Tyr Asn Met Thr Ser Glu Phe Glu Glu Met Leu Gln				
213	735	740	745	750	
215	gtc gga aac ctg gtc ttc aca ggg att ttc aca gca gag atg acc ttc				2307
216	Val Gly Asn Leu Val Phe Thr Gly Ile Phe Thr Ala Glu Met Thr Phe				
217	755	760	765		
219	aag atc att gcc ctc gac ccc tac tac ttc caa cag ggc tgg aac				2355
220	Lys Ile Ile Ala Leu Asp Pro Tyr Tyr Phe Gln Gln Gly Trp Asn				
221	770	775	780		
223	atc ttc gac agc atc atc gtc atc ctt agc ctc atg gag ctg ggc ctg				2403
224	Ile Phe Asp Ser Ile Ile Val Ile Leu Ser Leu Met Glu Leu Gly Leu				
225	785	790	795		
227	tcc cgc atg agc aac ttg tcg gtc ctg cgc tcc ttc cgc ctg ctg cgg				2451
228	Ser Arg Met Ser Asn Leu Ser Val Leu Arg Ser Phe Arg Leu Leu Arg				
229	800	805	810		
231	gtc ttc aag ctg gcc aaa tca tgg ccc acc ctg aac aca ctc atc aag				2499
232	Val Phe Lys Leu Ala Lys Ser Trp Pro Thr Leu Asn Thr Leu Ile Lys				
233	815	820	825	830	
235	atc atc ggg aac tca gtc ggg gca ctg ggg aac ctg aca ctg gtc cta				2547
236	Ile Ile Gly Asn Ser Val Gly Ala Leu Gly Asn Leu Thr Leu Val Leu				
237	835	840	845		
239	gcc atc atc gtc ttc atc ttt gtc gtc ggc atg cag ctc ttt ggc				2595
240	Ala Ile Ile Val Phe Ile Phe Ala Val Val Gly Met Gln Leu Phe Gly				
241	850	855	860		
243	aag aac tac tcg gag ctg agg gac agc gac tca ggc ctg ctg cct cgc				2643
244	Lys Asn Tyr Ser Glu Leu Arg Asp Ser Asp Ser Gly Leu Leu Pro Arg				
245	865	870	875		
247	tgg cac atg atg gac ttc ttt cat gcc ttc ctc atc atc ttc cgc atc				2691
248	Trp His Met Met Asp Phe Phe His Ala Phe Leu Ile Ile Phe Arg Ile				
249	880	885	890		
251	ctc tgt gga gag tgg atc gag acc atg tgg gac tgc atg gag gtc tcg				2739
252	Leu Cys Gly Glu Trp Ile Glu Thr Met Trp Asp Cys Met Glu Val Ser				
253	895	900	905	910	
255	ggg cag tca tta tcg ctg gtc ttc ttg ctt gtt atg gtc att ggc				2787
256	Gly Gln Ser Leu Cys Leu Leu Val Phe Leu Leu Val Met Val Ile Gly				
257	915	920	925		

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259 aac ctt gtg gtc ctg aat ctc ttc ctg gcc ttg ctg ctc agc tcc ttc	2835
260 Asn Leu Val Val Leu Asn Leu Phe Leu Ala Leu Leu Ser Ser Phe	
261 930 935 940	
263 agt gca gac aac ctc aca gcc cct gat gag gac aga gag atg aac aac	2883
264 Ser Ala Asp Asn Leu Thr Ala Pro Asp Glu Asp Arg Glu Met Asn Asn	
265 945 950 955	
267 ctc cag ctg gcc ctg gcc cgc atc cag agg ggc ctg cgc ttt gtc aag	2931
268 Leu Gln Leu Ala Leu Ala Arg Ile Gln Arg Gly Leu Arg Phe Val Lys	
269 960 965 970	
271 cgg acc acc tgg gat ttc tgc tgt ggt ctc ctg cgg cag cgg cct cag	2979
272 Arg Thr Thr Trp Asp Phe Cys Cys Gly Leu Leu Arg Gln Arg Pro Gln	
273 975 980 985 990	
275 aag ccc gca gcc ctt gcc gcc cag ggc cag ctg ccc agc tgc att gcc	3027
276 Lys Pro Ala Ala Leu Ala Ala Gln Gln Leu Pro Ser Cys Ile Ala	
277 995 1000 1005	
279 acc ccc tac tcc ccg cca ccc cca gag acg gag aag gtg cct ccc acc	3075
280 Thr Pro Tyr Ser Pro Pro Pro Glu Thr Glu Lys Val Pro Pro Thr	
281 1010 1015 1020	
283 cgc aag gaa aca cgg ttt gag gaa ggc gag caa cca ggc cag ggc acc	3123
284 Arg Lys Glu Thr Arg Phe Glu Glu Gly Glu Gln Pro Gly Gln Gly Thr	
285 1025 1030 1035	
287 ccc ggg gat cca gag ccc gtg tgt gtg ccc atc gct gtg gcc gag tca	3171
288 Pro Gly Asp Pro Glu Pro Val Cys Val Pro Ile Ala Val Ala Glu Ser	
289 1040 1045 1050	
291 gac aca gat gac caa gaa gaa gat gag gag aac agc ctg ggc acg gag	3219
292 Asp Thr Asp Asp Gln Glu Asp Glu Glu Asn Ser Leu Gly Thr Glu	
293 1055 1060 1065 1070	
295 gag gag tcc agc aag cag gaa tcc cag cct gtg tcc ggt ggc cca gag	3267
296 Glu Glu Ser Ser Lys Gln Glu Ser Gln Pro Val Ser Gly Gly Pro Glu	
297 1075 1080 1085	
299 gcc cct ccg gat tcc agg acc tgg agc cag gtg tca gcg act gcc tcc	3315
300 Ala Pro Pro Asp Ser Arg Thr Trp Ser Gln Val Ser Ala Thr Ala Ser	
301 1090 1095 1100	
303 tct gag gcc gag gcc agt gca tct cag gcc gac tgg cgg cag cag tgg	3363
304 Ser Glu Ala Glu Ala Ser Ala Ser Gln Ala Asp Trp Arg Gln Gln Trp	
305 1105 1110 1115	
307 aaa gcg gaa ccc cag gcc cca ggg tgc ggt gag acc cca gag gac agt	3411
308 Lys Ala Glu Pro Gln Ala Pro Gly Cys Gly Glu Thr Pro Glu Asp Ser	
309 1120 1125 1130	
311 tgc tcc gag ggc agc aca gca gac atg acc aac acc gct gag ctc ctg	3459
312 Cys Ser Glu Gly Ser Thr Ala Asp Met Thr Asn Thr Ala Glu Leu Leu	
313 1135 1140 1145 1150	
315 gag cag atc cct gac ctc ggc cag gat gtc aag gac cca gag gac tgc	3507
316 Glu Gln Ile Pro Asp Leu Gly Gln Asp Val Lys Asp Pro Glu Asp Cys	
317 1155 1160 1165	
319 ttc act gaa ggc tgt gtc cgg cgc tgt ccc tgc tgt gcg gtg gac acc	3555
320 Phe Thr Glu Gly Cys Val Arg Arg Cys Pro Cys Cys Ala Val Asp Thr	
321 1170 1175 1180	
323 aca cag gcc cca ggg aag gtc tgg tgg cgg ttg cgc aag acc tgc tac	3603

**VERIFICATION SUMMARY**

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DATE: 03/04/2002

TIME: 14:55:08

Input Set : A:\Sequence.app

Output Set: N:\CRF3\03042002\J077054.raw

L:10 M:270 C: Current Application Number differs, Replaced Application Number  
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date